

Db 241 LRLAKNRYLVLEANPNFVLPHTLDADAILLVYGRGALKMIRHNRRESYNLECGDVI 300
|||
QY 241 LRLAKNRYLVLEANPNFVLPHTLDADAILLVYGRGALKMIRHNRRESYNLECGDVI 300
Db 301 RIRAGTFFYLINRDNNEHLIAKFLQISTPGQYKEFFPAGGONPEPYLSTFSKEILEEA 360
|||
QY 301 RIRAGTFFYLINRDNNEHLIAKFLQISTPGQYKEFFPAGGONPEPYLSTFSKEILEEA 360
Db 361 LNTQTERLRLGVGLGOOREGVIIRASQEIIRLRTDRDSESRMHIRRGESSRGPYNLFNKR 420
|||
QY 361 LNTQTERLRLGVGLGOOREGVIIRASQEIIRLRTDRDSESRMHIRRGESSRGPYNLFNKR 420
Db 421 PLYSNKYGAYEVKPEPDYRQLODMVSVFIANTTQSGMGPFFNTSTKYVVAASGEADV 480
|||
QY 421 PLYSNKYGAYEVKPEPDYRQLODMVSVFIANTTQSGMGPFFNTSTKYVVAASGEADV 480
Db 481 EMACPHLSGRHGRGGKRHEEEEDVHYEQVARKLSKRAIYVYVGHVYVSSGNENLL 540
|||
QY 481 EMACPHLSGRHGRGGKRHEEEEDVHYEQVARKLSKRAIYVYVGHVYVSSGNENLL 540
Db 541 LFAFGINAQNNHENFLAGREERNVLOQIEPQAMELAFASRKEVEELFNSODESIFFPGPR 600
|||
QY 541 LFAFGINAQNNHENFLAGREERNVLOQIEPQAMELAFASRKEVEELFNSODESIFFPGPR 600
Db 601 QHQOQSPRSTKQOQPLVSLIDPVGF 625
|||
QY 601 QHQOQSPRSTKQOQPLVSLIDPVGF 625

RESULT 2

ID W62829 standard; Protein: 666 AA.
AC W62829;
DT 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note= "signal peptide"
FT 29..666
FT Protein /note= "mature protein"
PN MO9827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42311.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1, Page 39-41; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 666 AA;

Query Match 97.1%; Score 4496; DB 1; Length 666;
Best local Similarity 96.6%; Pred. No. 0.00e+00;
Matches 604; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Db 42 QCMQLETSGMRRCVSCQDKRFEDIDMSKYNDQDDPOTDCQOCQRCRQOESGPRQOY 101
|||
QY 1 QCMQLETSGMRRCVSCQDKRFEDIDMSKYNDQDDPOTDCQOCQRCRQOESDPRQOY 60
Db 102 CORKEICEEEEEYNNRQDPQOYEQCCORCRHETEPHNMOTCOQRCERYEKEKRQ 161
|||
QY 61 CORKEICEEEEEYNNRQDPQOYEQCCORCRHETEPHNMOTCOQRCERYEKEKRQ 120
Db 162 OKRYEEOQREDEKYEERKKEENDKRDPOQREYEDCRRCRQEOQEPQOYOCORCEQR 221
|||
QY 121 OKRYEEOQREDEKYEERKKEENDKRDPOQREYEDCRRCRQEOQEPQOYOCORCEQR 180

Db 222 QHGRGDLINPORGSGRGYEEGEKOSDNPPYFDERSLSTRTERGHISVLENYGRSK 281
|||
QY 181 QHGRGDLINPORGSGRGYEEGEKOSDNPPYFDERSLSTRTERGHISVLENYGRSK 240
Db 282 LRLAKNRYLVLEANPNFVLPHTLDADAILLVYGRGALKMIRHNRRESYNLECGDVI 341
|||
QY 282 LRLAKNRYLVLEANPNFVLPHTLDADAILLVYGRGALKMIRHNRRESYNLECGDVI 300
Db 342 RIRAGTFFYLINRDNNEHLIAKFLQISTPGQYKEFFPAGGONPEPYLSTFSKEILEEA 401
|||
QY 301 RIRAGTFFYLINRDNNEHLIAKFLQISTPGQYKEFFPAGGONPEPYLSTFSKEILEEA 360
Db 402 LNTQTERLRLGVGLGOOREGVIIRASQEIIRLRTDRDSESRMHIRRGESSRGPYNLFNKR 461
|||
QY 361 LNTQTERLRLGVGLGOOREGVIIRASQEIIRLRTDRDSESRMHIRRGESSRGPYNLFNKR 420
Db 462 PLYSNKYGAYEVKPEPDYRQLODMVSVFIANTTQSGMGPFFNTSTKYVVAASGEADV 521
|||
QY 421 PLYSNKYGAYEVKPEPDYRQLODMVSVFIANTTQSGMGPFFNTSTKYVVAASGEADV 480
Db 522 EMACPHLSGRHGRGGKRHEEEEDVHYEQVARKLSKRAIYVYVGHVYVSSGNENLL 581
|||
QY 481 EMACPHLSGRHGRGGKRHEEEEDVHYEQVARKLSKRAIYVYVGHVYVSSGNENLL 540
Db 582 LFAFGINAQNNHENFLAGREERNVLOQIEPQAMELAFASRKEVEELFNSODESIFFPGPR 641
|||
QY 541 LFAFGINAQNNHENFLAGREERNVLOQIEPQAMELAFASRKEVEELFNSODESIFFPGPR 600
Db 642 QHQOQSPRSTKQOQPLVSLIDPVGF 666
|||
QY 601 QHQOQSPRSTKQOQPLVSLIDPVGF 625

RESULT 3

ID W62828 standard; Protein: 666 AA.
AC W62828;
DT 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
FH Key Location/Qualifiers
FT Peptide 1..28
FT /note= "signal peptide"
FT 29..666
FT Protein /note= "mature protein"
PN MO9827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42310.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1, Page 34-36; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 666 AA;

Query Match 96.9%; Score 4487; DB 1; Length 666;
Best local Similarity 96.6%; Pred. No. 0.00e+00;
Matches 604; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Db 42 QCMQLETSGMRRCVSCQDKRFEDIDMSKYNDQDDPOTDCQOCQRCRQOESGPRQOY 101
|||
QY 1 QCMQLETSGMRRCVSCQDKRFEDIDMSKYNDQDDPOTDCQOCQRCRQOESDPRQOY 60
Db 102 CORKEICEEEEEYNNRQDPQOYEQCCORCRHETEPHNMOTCOQRCERYEKEKRQ 161
|||
QY 61 CORKEICEEEEEYNNRQDPQOYEQCCORCRHETEPHNMOTCOQRCERYEKEKRQ 120

D	b	156	PWGE-REEADEEBET--EGGQDSHPNPFHHRKRSFOSRRREHGNGRVLQFARASHRPL	213
O	y	183	GGGGLMPPQGGSGGRVEEGEKEKSDMPYFDERLSLSTRTEBGHATSVLENYGRKLL	242
D	b	214	RGINEFRLSLEAMPNPFVLRPHCDAEKIVYLTNGRSTLFLTHENKESYNIYGVVVKY	273
O	y	243	RALKNYRVLLEAMPNPFVLRPHDADAILLYIGGRALKMIRHNDNESINLECGVIAR	302
D	b	274	PAGTIVYIANDONEKELLIAVLHPVPNNPGOFEEFPFAGSORPOSITYRAFSSRIELEPAEN	333
O	y	303	PAGTIFYIINDNDRERLHIAFLTQISTPGCYKEFFPAGGONDEPYSLTSTKSKEILAAIN	362
D	b	334	TRSEOLDLFGGRRSRROOQGGFRASQOIRALSOEAT--SPR-E--KSGE--EFAFN	387
O	y	363	TQTERLRGVLC--Q--QRE-G-VIIR-ASQOIRELTRDSESKRWHIRRGSSSGPYN	415
D	b	388	LLSOTPRYSNONGRFFFEACPEEPFROLADINVTYSAQLNOSIFVPHYNSKATFVILYTE	447
O	y	416	LFNKRLPTSNKYGAAVEKPEPDYRQLDMQVSVIANITQSGMMGPFENRSTRKTVVVAS	475
D	b	448	GNGVAAEMWSPLPROSSVEEBEEDDEEDQOEERRSQGYRKIRISLSTSGDLFFVVPANF	507
O	y	476	GEADVEMACPHL---SG--RHGGRGGRKRHEEBE--V--HYEVRALRSKREIAIVVLAGH	527
D	b	508	PVTEVASONQLRMATGGGLYNQONINPDHONIRIYFAGKINNY--RQWDSQAETELAFVSSRL	566
O	y	528	PVFEVSSGNEKULLFARGINQN--N--H--EN-FLAGERNVLDQIEPQAMELAFASRKE	582
D	b	567	VDLEFNSNPDESYFVS--RQKORAS	569
O	y	583	VEELFNSODESIFPPGPRQHOOS	606

RESULT 6
ID W62831 standard; Protein; 525 AA.
AC W62831;
DT 27-OCT-1998 (first entry)
DE Theobroma cacao antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Theobroma cacao.
PN MO9827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PT (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PA Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
WP1: 98-377219/32.
DR Novel anti-microbial protein from e.g. *Macadamia integrifolia* -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 47-49; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 525 AA;

Query Match	24.8%	Score 1149	DB 1	Length 525
Best Local Similarity	40.4%	Pred. No. 3.90e-91		
Matches	133	Conservative 121	Mismatches 141	Indels 23
				Gaps 17

[illegible]

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QY 272 LLYIGRGALKKMIHFDNEESINLECGDVIIRIPACTTFLYLRNDRNRLHIAKFLQITISTP 331
Db 266 GKYLEFPFAGANNRPESYGAESTYLEVLEVTFTQREKELEIEBORGORQOOGQOMGRKA 325
QY 333 GQYKEFFPAGGONPPPYLSTSEKLEALMALTQTERLGRVGGQOREVIIIRASGEQIREL 391
Db 326 KPEQJRAISQATSPRHNGFERLAINLISQSPVSNONGRFEKCPDEFSQOMDVAVS 385
QY 392 TRDD--SSRRHRLIRGESESRGPNLNEKRPILSNKYGAEVXKPEYRLOLOMDVSF 448
Db 386 AELKNGDAIFPPHYNSKATFVVTYDYGAYQAMCAPHLSSQSGOSGRODRREQDESE 445
QY 450 IANITOGSMGPFETRSTKTVVVAASGADVEMACPHLSGR-HGCRGG--GKR-HEEE-- 503
Db 446 EHTFEEDPOVAPLPSGQVFAAPAGHANTFASADQPLNVAFAELNNONNORITLAA 503
QY 504 EEV--HYQVRRRLSRKRAIIVLGLHPVAVSSQENENILFAPFINNONNENLAA 559

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RESULT 7
ID W62835 standard; Protein; 593 AA.
AC W62835;
DT 27-OCT-1998 (first entry)
DE Zea mays antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Zea mays.
PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1987; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR.) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPtI. 98-377279/32.
PT Novel anti-microbial protein from e.g. *Macadamia integrifolia* - a
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1, Page 56-60; 6pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 593 AA;

Query Match	23.2%;	Score 1073;	DB 1;	Length 593;
Best Local Similarity	40.8%;	Pred. No. 3.83e-84;		
Matches	204;	Conservative	109;	Mismatches 158;
			Indels	29;
			Gaps	22;

Db	25	EDDNHHHGHKSQCVCARCEDR-PMHQRPRLCQCEEREKERKQERSRHEADRSGEGS	83
Oy	141	EGDNKRDEQOQREYEDCECRHCEQOQPRLOY-OCORRCEOORO - HGSGQILMNPQRG - GS	196
Db	84	SEDEEOEKEROKXRPVPVPRBSRFRVSVSEOSLVLNRPDEVSLLGINDYPAVL	143
Oy	197	GRYE-EGE-EKOSDN-PLYPDERLSLSTRFRTEBQHSIVLENFGRSLKLLAALKNYRLVLL	253
Db	144	EANPSEFVPSPTDAHCICVAAEGEVVTTIENERSYTIKQGHVAPARAVTYLANT	203
Oy	254	EANPRAFLPLHLDADAILLYIGRALKMIHMRNRSYNLECGDVIRIPAGTFTYLNR	313
Db	204	DGRKLVYTKLMTI SVPGEOFPPFGGRNPSEFLSSFEKSITORAAYKTSODRLERLFG	263
Oy	314	DNNEHLTHAKELQITSPGQYKEFFPAGGNQPEBYLSTFEKELLEALINTQTERLVLG	373
Db	264	RHGODKGIIVATEOQREILBRNASEGCHGNMPLPFGES-NGPVSLLORPSIANOHG	322
Oy	374	QO-RE-GVILRASEOQLRELLRDDSSE-R-RWHIRRGESSRCPVLENKRPVLSKYIG	428
Db	323	QLYEADANSFHDLEHADVSVSFANITAGSMAPLFTNRSKRIAYVPNGKQYAEIVCPHRO	382
Oy	429	QAYEVKPEDYHQLODMDOVSVEIANITGSMNGPPEFNTRSKVYVVASGEADVEMACH-L	487
Db	363	SQSGESEFERDKGRSRSEEESESESEDEEAKQGYHTTRAFLSQCTAFVVPAGHPVAANS	442
Oy	488	S-GRNGG-G-GGR-----HE--EE-EV-H-YEQVRAKSLREALVYLAGHPVVVS	534


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OY 442 QDMVSVFIANTOGSMGPFENTRSTKVYVVASGEADVEMACPHLSGRHGGGGRHE 501
DB 398 KSSPS-YHRISDDLKPGWVFPVPGHPTVITASNKENLMICEVARNDK-KFPFAGD 455
OY 502 EEEVHYEVARLRSKREAIYVLAGHPVYVSSGNNLLFAGINAKNNHENF-LAGNE 560
DB 456 -NIVSSLDNVAKEAFNYPSEMVNGVF 481
OY 561 RNVLQOIEPQAMELAFASRKEVEELF 587

RESULT 10
ID W62838 standard; protein: 605 AA.
AC W62838;
DE 27-OCT-1998 (first entry)
KW Glycine max antimicrobial protein.
OS antimicrobial protein; infestation; control.
PN Glycine max.
PD WO9827805-A1.
PE 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (REIR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JT, Manners JM, Marcus JP;
DR WPI: 98-37729/32.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PR useful for controlling microbial infestations of plants or mammals
CC Claim 1: Page 63-65: 96pp: English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 605 AA:

Query Match 21.0%; Score 972; DB 1; Length 605;
Best Local Similarity 32.8%; Pred. No. 7,086-75;
Matches 194; Conservative 162; Mismatches 194; Indels 41; Gaps 32;

DB 38 CLOSC-NSESDSYRNQACHARNLKEKECEGEIPRR-PRQHP-EREPOQGEKE 94
OY 44 CORRCROESDPRQOYQCRCKEICEEEENRQDRPOQYEQCRQCRRETEPRHMQ 103
DB 95 EDEDE-QPR-PIPFPRQPR-QEEHEORE-QEWPBK-EERKGECSSED-EDEDEQ 148
OY 104 ICQQRCEERYEKEKRRQOQRYEQREDEKYEERKEDNDRDPOQREYECRRHCEQ 163
DB 149 DER-OFPPRPHPQKEERNEEDEDQOQSEES-EDSELRRKNNKPNFLGSRNFETL 206
OY 164 EERLQYQORQROEOORHGRGDLMPORGSGRYEGBE-EKQSD-NPYTFDESLSTR 221
DB 207 FKNQYGRIVLQRFNORSFQLONLDRYILFENSKPNTLLPNNADADYLVILNGTAL 266
OY 222 FRTGEGHISVLENFYGRSKLLRALKNYRLVLEAPNNAFVLPJHDAADAILVIGRGAL 281
DB 267 SLVNNDDDSYLOGSDALRVPSGTTYVYVNDNNENLRLLTALPYNKGPFESFELS 326
OY 282 KNIHNDNRSYVLECGDVIRIPAGTFYILINDNNEERLHIAFLQTIISTPGQYKKEFFPAG 341
DB 327 TEAOQSYLOGFRNILEASDYTKFEEINKVLFRESGOQOGEORLOESYVISEKQIRA 386
OY 342 GONPEPLYSTKEKLEALANTQ-TE--R-L--R--GV-L-GQOR--EGYITASQOIRHE 390
DB 387 LSKRAKSSSRK-TI--SSED-K-PENLRSRDPISYNNKLKFEFETPEKNPQDRDDIFLS 441
OY 391 LT-RDDESERRWHIRGGSSRGPNLFFNKRLPLYSKNYGOAEVPEDEYRQLODMVSYF 449
DB 442 IVDNMEGALLLPHFNSKALVILYINBEGANIELV-G-LKEQOQEO---QOEOPLEVR-- 494
OY 450 IANITQGSMMGPFENTRSTKVYVVASGEADVEMACPHLSGRHGGGGRHEEEVHYE 509
DB 495 KRAEISEODIVIPAGYVYV-VNATS--NLNFEAIGINANNORNLGASQONVISOIPS 552
OY 510 QVRALRSKREAIYVLAGHPVYVSSGNNLLFAGINAKNNHENF-LAGREKNVLAQOIEP 569
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DB 553 QVOELAFPGSAQAVEKLKNQRESYFVDAQPKKKEGNGKRGK--PLSSIL 601
OY 570 QAMELAFASRKEVEELFNSQDESIFFPGRHQOQSPRSTKQOQPLVSIL 620

RESULT 11
ID W90340 standard; protein: 444 AA.
AC W90340;
DE 24-MAY-1999 (first entry)
KW G. max truncated SBP1 protein.
DE SBP1; sucrose binding protein. SBP2; sucrose uptake; transgenic plant;
KW seed; carbohydrate content; soybean.
OS Glycine max.
PN WO9853086-A1.
PD 26-NOV-1998.
PR 21-MAY-1998; U10465.
PR 22-MAY-1997; US-047568.
PA (UNIV) UNIV WASHINGTON STATE RES FOUND.
PI Chao WS, Grimes HD;
DR WPI: 99-070155/06.
PT New modified plant; sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds.
PR Claim 7: Page 36-37: 58pp: English.
CC This sequence represents a novel sucrose binding protein, SBP1 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
SQ Sequence 444 AA:

Query Match 20.2%; Score 934; DB 1; Length 444;
Best Local Similarity 38.2%; Pred. No. 2,136-71;
Matches 156; Conservative 112; Mismatches 112; Indels 19; Gaps 17;

DB 49 QOQOYTEDKRVYCQSDCRHYRMKQER-EKOIOETREKKEESREREDEQ-EQHEE-Q 105
OY 149 QQREY-EDCRHHCQOEPRLQYQCRQCEQOQROHGRG-DLMPORGSGRYEGEEO 206
DB 106 DENPIFEEDDFETRVETEGGRIVLKKFTEKSKLLOGENFRALTEARAFVSPRH 165
OY 207 SDNPYTFDE-KLSLSTRFTEGHSVLENFYGRSKLLRALKNYRLVLEAPNNAFVLP 265
DB 166 FDSEVVEFNIGRAVLGVSESETEKITLEPDMIHIPAGTPLYIVNDENDKFLAMLH 225
OY 266 LDADAIIIVIGRGALKMHIHNDNRSYVLECGDVIRIPAGTFYILINDNNEERLHIAKF 324
DB 226 IPVSVSTGKFEFFPARGRPESVLSFWMNVQALQOTKGLNVFDQONGSIFRI 285
OY 325 LQ-TISTPGQYKEFFPAGQNPDEYLSFESKEILEALANTQTERLQVLOGOORGVYIRA 383
DB 286 SREQVRLAPTKKSSW-WPF--GGES-KPQENISKRPTISNGVGRLEVEPPDDDEKSWL 341
OY 384 SQEQIRELTRDSESRRHNRHGRGESSRGPNLNNKRLPLYSKNYGOAEVAPEDY-RQ-L 441
DB 442 QRLNMLTFTNORSMTIHYNSHAKIALVIDGRGLQISCPHMSR-SSHS--R-HD 397
OY 442 QDMVSVFIANTOGSMGPFENTRSTKVYVVASGEADVEMACPHLSGRHGGGGRHE 501
DB 398 KSSPS-YHRISDDLKPGWVFPVPGHPTVITASNKENLMICEVARNDK-KFPFAGD 455
OY 502 EEEVHYEVARLRSKREAIYVLAGHPVYVSSGNNLLFAGINAKNNHENF-LAGNE 549
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